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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/029,756

DATE: 01/18/2002

TIME: 09:18:30

Input Set : N:\Crf3\RULE60\10029756.raw
 Output Set: N:\CRF3\01182002\J029756.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Thomas, Terry L.

8 (ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
9 DELTA 6-DESATURASE

11 (iii) NUMBER OF SEQUENCES: 27

13 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Scully, Scott, Murphy & Presser

16 (B) STREET: 400 Garden City Plaza

17 (C) CITY: Garden City

18 (D) STATE: New York

19 (E) COUNTRY: United States

20 (F) ZIP: 11530

22 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/10/029,756

C--> 32 (B) FILING DATE: 21-Dec-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/934,254

38 (B) FILING DATE:

42 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Presser, Leopold

45 (B) REGISTRATION NUMBER: 19,827

46 (C) REFERENCE/DOCKET NUMBER: 8383ZYXWVU

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (516) 742-4343

50 (B) TELEFAX: (516) 742-4366

51 (C) TELEX: 230 901 SANS UR

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 3588 base pairs

58 (B) TYPE: nucleic acid

59 (C) STRANDEDNESS: both

60 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: DNA (genomic)

64 (ix) FEATURE:

66 (A) NAME/KEY: CDS

67 (B) LOCATION: 2002..3081

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69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71  GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCG GTATTCTGAA      60
73  TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC      120
75  CACCTTCCCA CACCCAGCTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTCCTT      180
77  TCGCGGCTTG GCGCAATCAGG CGATCGGGCA ATTGCGTTTG TTTGACCAGA CTTTGGCCCAT      240
79  TCAGGAAATT GTCAATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTATG      300
81  GGATGATCGG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTTAGT      360
83  AGGCGCAGTG GTGAATAATT TAACGTGGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA      420
85  ACCCCAAACC AAGACCAAAAC GCGGATCGCC TTGGGCGAAA TTTTCCAAAC TGATTACCAC      480
87  CCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTGTG TTTTATTGTT      540
89  GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGA      600
91  CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGCCCGGT GGCAAGGAAG AGGTGGCCGA      660
93  AAAATCCCCC GATAATCATCA AAGTATTCCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT      720
95  GATTGGTATT TGTTATGCCC TACTGAATGA TTTCATCCTT GGCAGTCGCT TTTGATCAGTT      780
97  TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGCG TGGGGGGAGT      840
99  GAGCATGGCC ATTTATTGAG AGTTAATTCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA      900
101 GGATACAGAT AATCGTTTCT TGCATACGGC CCGCTCCCTG GGGGTGCCCG TAATTGTGGA      960
103 GATGTCGCCG CTAGAAAGAA CGTTGGCCTG GCCTAATATC AACCGAGCCG AAGCCATTCT      1020
105 GTGGGCCACC AGCGACGACA CCGTTAACTT GGAATTTGGC CTAACGTCCA AGCGCATCGC      1080
107 CCTTGGCTTG CCAAGTGGTG TGCGTTGCCA GGATGCCCAG TTTAGCCTGT CCTCGCAGGA      1140
109 AGTATTTGAA TTTGAAACGG TGCTTTGTCC GGGCGAATTG GCCACCTATT CCTTTGCGCG      1200
111 GCGCGCCCTG GGGGGCAAAA TTTTGGGCAA CGCATGACC GATGATTTCG TGTGGGTAGC      1260
113 CTAGCCACC TTAATCACTC CTAACCATCC CTTTGCCGAC AGACGTTGTT CAATTGGTTA      1320
115 CCAAAGTCT GATTTCGTTC CCCTCTATCT AGAACGGGGT GGCAAAACCA TCCATAGCTG      1380
117 GGAATTATTG GTTACCCATC TCGACTCTGG AGACGTTGTT TATTTAACCA TGCCCGCCAC      1440
119 TGCTCTATGT CAACITTTGGC GATCGCCCCG TGCCACTGCT GATCCTCTGG ACTCTTTTTT      1500
121 GGTCTTAGAT GGGGGGATGG AACTCTTGAC TCGGCCCAAT GGTGATCAAG AAAGAACGCT      1560
123 TTGCTATGTG TTAGTATTTT TAAGTTAAOC AACAGCAGAG GATAACTTCC AAAAGAAATT      1620
125 AAGCTCAAAA AGTAGCAAAA TAAGTTTAAAT TCATACTGA GTTTTACTG TAAACAGCGG      1680
127 TGCAAAAAAG TCAGATAAAA TAAAGGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC      1740
129 CAGGCATCTG CTCTAGGGAG TTTTCCCGCT GCCTTTAGAG AGTATTTTCT CCAAGTCGGC      1800
131 TAACTCCCCC ATTTTATAGC AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG      1860
133 ATGACTCACT GTAGAAGGCA GACTAAAAAT CTAGCAATGG ACTCCCATGT GGAATAAAAT      1920
135 TTTAGTCTCC CCGCGCGCTG GAGTTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTTT      1980
137 TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC      2031
138 Met Leu Thr Ala Glu Arg Ile Lys Phe Thr
139 1 5 10
141 CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC      2079
142 Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr
143 15 20 25
145 TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC ATG TAT CTG
146 Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu      2127
147 30 35 40
149 AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GC TTT GTG
150 Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val      2175
151 45 50 55
153 CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT
154 Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys Met Val      2223
155 60 65 70

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157	TTG	GCG	ATC	GCC	TTG	GCG	GCC	TTT	TCC	TTC	AAT	GTC	GGC	CAC	GAT	GCC	2271
158	Leu	Ala	Ile	Ala	Leu	Ala	Ala	Phe	Ser	Phe	Asn	Val	Gly	His	Asp	Ala	
159	75					80					85					90	
161	AAC	CAC	AAT	GCC	TAT	TCC	TCC	AAT	CCC	CAC	ATC	AAC	CGG	GTT	CTG	GGC	2319
162	Asn	His	Asn	Ala	Tyr	Ser	Ser	Asn	Pro	His	Ile	Asn	Arg	Val	Leu	Gly	
163					95					100					105		
165	ATG	ACC	TAC	GAT	TTT	GTC	GGG	TTA	TCT	AGT	TTT	CTT	TGG	CGC	TAT	CGC	2367
166	Met	Thr	Tyr	Asp	Phe	Val	Gly	Leu	Ser	Ser	Phe	Leu	Trp	Arg	Tyr	Arg	
167					110					115				120			
169	CAC	AAC	TAT	TTG	CAC	CAC	ACC	TAC	ACC	AAT	ATT	CTT	GGC	CAT	GAC	GTG	2415
170	His	Asn	Tyr	Leu	His	His	Thr	Tyr	Thr	Asn	Ile	Leu	Gly	His	Asp	Val	
171					125					130				135			
173	GAA	ATC	CAT	GGA	GAT	GGC	GCA	GTA	CGT	ATG	AGT	CCT	GAA	CAA	GAA	CAT	2463
174	Glu	Ile	His	Gly	Asp	Gly	Ala	Val	Arg	Met	Ser	Pro	Glu	Gln	Glu	His	
175					140					145				150			
177	GTT	GGT	ATT	TAT	CGT	TTC	CAG	CAA	TTT	TAT	ATT	TGG	GGT	TTA	TAT	CTT	2511
178	Val	Gly	Ile	Tyr	Arg	Phe	Gln	Gln	Phe	Tyr	Ile	Trp	Gly	Leu	Tyr	Leu	
179	155					160					165			170			
181	TTC	ATT	CCC	TTT	TAT	TGG	TTT	CTC	TAC	GAT	GTC	TAC	CTA	GTG	CTT	AAT	2559
182	Phe	Ile	Pro	Phe	Tyr	Trp	Phe	Leu	Tyr	Asp	Val	Tyr	Leu	Val	Leu	Asn	
183						175					180				185		
185	AAA	GGC	AAA	TAT	CAC	GAC	CAT	AAA	ATT	CCT	CCT	TTC	CAG	CCC	CTA	GAA	2607
186	Lys	Gly	Lys	Tyr	His	Asp	His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu	
187						190					195			200			
189	TTA	GCT	AGT	TTG	CTA	GGG	ATT	AAG	CTA	TTA	TGG	CTC	GGC	TAC	GTT	TTC	2655
190	Leu	Ala	Ser	Leu	Leu	Gly	Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe	
191						205					210			215			
193	GGC	TTA	CCT	CTG	GCT	CTG	GGC	TTT	TCC	ATT	CCT	GAA	GTA	TTA	ATT	GGT	2703
194	Gly	Leu	Pro	Leu	Ala	Leu	Gly	Phe	Ser	Ile	Pro	Glu	Val	Leu	Ile	Gly	
195						220					225			230			
197	GCT	TCG	GTA	ACC	TAT	ATG	ACC	TAT	GGC	ATC	GTG	GTT	TGC	ACC	ATC	TTT	2751
198	Ala	Ser	Val	Thr	Tyr	Met	Thr	Tyr	Gly	Ile	Val	Val	Cys	Thr	Ile	Phe	
199	235					240					245			250			
201	ATG	CTG	GCC	CAT	GTG	TTG	GAA	TCA	ACT	GAA	TTT	CTC	ACC	CCC	GAT	GGT	2799
202	Met	Leu	Ala	His	Val	Leu	Glu	Ser	Thr	Phe	Leu	Thr	Pro	Asp	Gly		
203						255					260			265			
205	GAA	TCC	GGT	GCC	ATT	GAT	GAC	GAG	TGG	GCT	ATT	TGC	CAA	ATT	CGT	ACC	2847
206	Glu	Ser	Gly	Ala	Ile	Asp	Asp	Glu	Trp	Ala	Ile	Cys	Gln	Ile	Arg	Thr	
207						270					275			280			
209	ACG	GCC	AAT	TTT	GCC	ACC	AAT	AAT	CCC	TTT	TGG	AAC	TGG	TTT	TGT	GGC	2895
210	Thr	Ala	Asn	Phe	Ala	Thr	Asn	Asn	Pro	Phe	Trp	Asn	Trp	Phe	Cys	Gly	
211						285					290			295			
213	GGT	TTA	AAT	CAC	CAA	GTT	ACC	CAC	CAT	CTT	TTC	CCC	AAT	ATT	TGT	CAT	2943
214	Gly	Leu	Asn	His	Gln	Val	Thr	His	His	Leu	Phe	Pro	Asn	Ile	Cys	His	
215						300					310						
217	ATT	CAC	TAT	CCC	CAA	TTG	GAA	AAT	ATT	ATT	AAG	GAT	GTT	TGC	CAA	GAG	2991
218	Ile	His	Tyr	Pro	Gln	Leu	Glu	Asn	Ile	Ile	Lys	Asp	Val	Cys	Gln	Glu	
219	315					320					325			330			
221	TTT	GGT	GTG	GAA	TAT	AAA	GTT	TAT	CCC	ACC	TTC	AAA	GCG	GCG	ATC	GCC	3039

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222 Phe Gly Val Glu Tyr Lys Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala
223      335      340      345
225 TCT AAC TAT CGC TGG CTA GAG GCC ATG GGC AAA GCA TCG TGACATTGCC      3088
226 Ser Asn Tyr Arg Trp Leu Glu Ala Met Gly Lys Ala Ser
227      350      355
229 TTGGGATTGA AGCAAAATGG CAAAATCCCT CGTAAATCTA TGATCGAAGC CTTTCTGTTG      3148
231 CCCGCCGACC AAATCCCCGA TGCTGACCAA AGGTTGATGT TGGCATTGCT CCAAACCCAC      3208
233 TTGAGGGGGG TTCATTGGCC GCAGTTTCAA GCTGACCTAG GAGGCAAAGA TTGGGTGATT      3268
235 TTGCTCAAAAT CCGCTGGGAT ATTGAAAGGC TTCACCACCT TTGGTTTCTA CCGTGTCTCAA      3328
237 TGGGAAGGAC AAACCGTCAG AATTGTTTAT TCTGGTGACA CCATCACCGA CCCATCCATG      3388
239 TGGTCTAACC CAGCCCTGGC CAAGGCTTGG ACCAAGGCCA TGCAAATTCT CCACGAGGCT      3448
241 AGGCCAGAAA AATTATATTG GCTCCTGATT TCTCCGCTCT ATCGCACCTA CCGATTTTTG      3508
243 AGCATTTTGT CCAAGGAATT CTATCCCCAC TATCTCCATC CCACTCCCCC GCCTGTACAA      3568
245 AATTTTATCC ATCAGCTAGC
248 (2) INFORMATION FOR SEQ ID NO: 2:
250 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 359 amino acids
253 (B) TYPE: amino acid
254 (D) TOPOLOGY: linear
256 (ii) MOLECULE TYPE: protein
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
260 Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
261 1      5      10      15
263 Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
264      20      25      30
266 Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu Lys Thr Leu Ile Ile Val
267      35      40      45
269 Leu Trp Leu Phe Ser Ala Trp Ala Phe Val Leu Phe Ala Pro Val Ile
270      50      55      60
272 Phe Pro Val Arg Leu Leu Gly Cys Met Val Leu Ala Ile Ala Leu Ala
273      65      70      75      80
275 Ala Phe Ser Phe Asn Val Gly His Asp Ala Asn His Asn Ala Tyr Ser
276      85      90      95
278 Ser Asn Pro His Ile Asn Arg Val Leu Gly Met Thr Tyr Asp Phe Val
279      100      105      110
281 Gly Leu Ser Ser Phe Leu Trp Arg Tyr Arg His Asn Tyr Leu His His
282      115      120      125
284 Thr Tyr Thr Asn Ile Leu Gly His Asp Val Glu Ile His Gly Asp Gly
285      130      135      140
287 Ala Val Arg Met Ser Pro Glu Gln Glu His Val Gly Ile Tyr Arg Phe
288      145      150      155      160
290 Gln Gln Phe Tyr Ile Trp Gly Leu Tyr Leu Phe Ile Pro Phe Tyr Trp
291      165      170      175
293 Phe Leu Tyr Asp Val Tyr Leu Val Leu Asn Lys Gly Lys Tyr His Asp
294      180      185      190
296 His Lys Ile Pro Pro Phe Gln Pro Leu Glu Leu Ala Ser Leu Leu Gly
297      195      200      205
299 Ile Lys Lys Leu Trp Leu Gly Tyr Val Phe Gly Leu Pro Leu Ala Leu
300      210      215      220
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302 Gly Phe Ser Ile Pro Glu Val Leu Ile Gly Ala Ser Val Thr Tyr Met
303 225 230 235 240
305 Thr Tyr Gly Ile Val Val Cys Thr Ile Phe Met Leu Ala His Val Leu
306 245 250 255
308 Glu Ser Thr Glu Phe Leu Thr Pro Asp Gly Glu Ser Gly Ala Ile Asp
309 260 265 270
311 Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr Thr Ala Asn Phe Ala Thr
312 275 280 285
314 Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly Gly Leu Asn His Gln Val
315 290 295 300
317 Thr His His Leu Phe Pro Asn Ile Cys His Ile His Tyr Pro Gln Leu
318 305 310 315 320
320 Glu Asn Ile Ile Lys Asp Val Cys Gln Glu Phe Gly Val Glu Tyr Lys
321 325 330 335
323 Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala Ser Asn Tyr Arg Trp Leu
324 340 345 350
326 Glu Ala Met Gly Lys Ala Ser
327 355
330 (2) INFORMATION FOR SEQ ID NO: 3:
332 (i) SEQUENCE CHARACTERISTICS:
334 (A) LENGTH: 1884 base pairs
335 (B) TYPE: nucleic acid
336 (C) STRANDEDNESS: both
337 (D) TOPOLOGY: linear
339 (ii) MOLECULE TYPE: DNA (genomic)
341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
343 AGCTTCACCT CGGTTTATATA TTGTGACCAT GGTCCCAGG CATCTGCTCT AGGGAGTTTT 60
345 TCCGCTGCCT TTAGAGAGTA TTTTCTCCAA GTCCGCTAAC TCCCCCATTT TTAGGCAAAA 120
347 TCATATACAG ACTATCCCAA TATTGCCAGA GCTTTGATGA CTCAGCTAGT AAGGCAGACT 180
349 AAAATTCTAG CAATGGACTC CCAGTTGGAA TAAATTTTTA GTCTCCCCCG CGCGTGGAGT 240
351 TTTTGTGTAG TTAATGGCGG TATAATGTGA AAGTTTTTTA TCTATTTAAA TTTATAAATG 300
353 CTAACAGCGG AAAGAATTAA ATTTACCCAG AACCGGGGGT TTGCTCGGTT ACTAAACCAA 360
355 CGGGTGGATG CCTACTTTGC CGAGCATGGC CTGACCCAAA GGGATAATCC CTCCATGTAT 420
357 CTGAAAACCC TGATTATTGT GCTCTGGTGT TTTTCCGCTT GGGCCTTTGT GCTTTTGTCT 480
359 CCAGTTATTT TTCCGGTGGG CCTACTGGGT TGTATGGTTT TGGCGATCGC CTTGGCGGCC 540
361 TTTTCTCTCA ATGTCCGCCA CGATGCCAAC CACAATGCCT ATTCCTCCAA TCCCCACATC 600
363 AACCCGGTTC TGGGCATGAC CTACGATTTT GTCGGGTTAT CTAGTTTTC TTTGGCGCTAT 660
365 CGCCACAACAT ATTTGCACCA CACCTACACC AATATTTCTT GCCATGAGT GGAAATCCAT 720
367 GGAGATGGGG CAGTACGTAT GAGTCTCGAA CAAGAACATG TTGGTATTTA TCGTTTCCAG 780
369 CAATTTTATA TTTGGGTTT ATATCTTTTC ATTCCTTTT ATTGGTTTCT CTACGATGTC 840
371 TACCTAGTGC TTAATAAAGG CAAATATCAC GACCATAAAA TTCTCCTTTT CCAGCCCCTA 900
373 GAATTAGCTA GTTTGCTAGG GATTAAAGCTA TTATGGCTCG GCTACGTTTT CGGCTTACCT 960
375 CTGGCTCTGG GCTTTTCCAT TCCTGAAGTA TTAATTGGTG CTTCCGTAAC CTATATGACC 1020
377 TATGCGCATC TGGTTTGCAC CATCTTTATG CTGGCCCATG TGTGGGAATC AACTGAATTT 1080
379 CTCACCCCGG ATGGTGAATC CGGTGCCATT GATGACGAGT GGGCTATTGT CCAATTCGT 1140
381 ACCACGGCCA ATTTTGGCAC CAATAATCCC TTTTGAACCT GGTTTTGTGG CGGTTTAAAT 1200
383 CACCAAGTTA CCCACCATCT TTTCCCAAT ATTTGTCTATA TTCACATACC CCAATTGGAA 1260
385 AATATTATTA AGGATGTTG CCAAGAGTTT GGTGTGGAAT ATAAAGTTTA TCCCACCTTC 1320
387 AAAGCGCGA TCGCCTCTAA CTATCGCTGG CTAGAGGCCA TGGGCAAAGC ATCGTGACAT 1380

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10029756.raw

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]